

**CLAIMS:**

- 1           1. An isolated polynucleotide sequence, comprising the sequence of SEQ ID NO 23.
  
- 1           2. An isolated polynucleotide sequence, comprising:  
2           a region of variable number tandem repeats including at least one sequence selected from  
3           the group consisting of SEQ ID NO 24, SEQ ID NO 25, SEQ ID NO 26, SEQ ID NO 27, SEQ  
4           ID NO 28, SEQ ID NO 29, SEQ ID NO 30, SEQ ID NO 31, SEQ ID NO 32, SEQ ID NO 33,  
5           SEQ ID NO 34, SEQ ID NO 35, and SEQ ID NO 36.
  
- 1           3. The isolated polynucleotide sequence according to claim 2, further comprising:  
2           at least one point mutation in at least one sequence.
  
- 1           4. The isolated polynucleotide sequence according to claim 3, wherein the number of  
2           point mutations is insufficient to prevent identification of the sequence and determination of  
3           phylogenetic relatedness of organisms including the sequence in their genome.
  
- 1           5. The isolated polynucleotide sequence according to claim 3, wherein the at least one  
2           point mutation is not in the first three nucleotides of the at least one sequence.
  
- 1           6. The isolated polynucleotide sequence according to claim 2, further comprising:  
2           a forward primer upstream of the sequence; and  
3           a reverse primer downstream of the sequence,

4            wherein the forward primer and the reverse primer permit identification of the region of  
5   variable number tandem repeats.

1            7. The isolated polynucleotide sequence according to claim 6, wherein the forward  
2   primer comprises SEQ ID NO 37 and the reverse primer comprises SEQ ID NO 38.

1            8. The isolated polynucleotide sequence according to claim 2, wherein the sequence  
2   comprises more than one copy of SEQ ID NO 24, SEQ ID NO 25, SEQ ID NO 26, SEQ ID NO  
3   27, SEQ ID NO 28, SEQ ID NO 29, SEQ ID NO 30, SEQ ID NO 31, SEQ ID NO 32, SEQ ID  
4   NO 33, SEQ ID NO 34, SEQ ID NO 35, or SEQ ID NO 36.

1            9. The isolated polynucleotide sequence according to claim 2, wherein the sequence  
2   codes for a protein sequence comprising:  
3        SEQ ID NO 39, SEQ ID NO 40, SEQ ID NO 41, SEQ ID NO 42, SEQ ID NO 43, SEQ  
4   ID NO 44, SEQ ID NO 45, SEQ ID NO 46, SEQ ID NO 47, and SEQ ID NO 48.

1            10. The isolated polynucleotide sequence according to claim 2, wherein the sequence is  
2   isolated from *Enterococcus faecalis*.

1            11. The isolated polynucleotide sequence according to claim 2, wherein the first three  
2   nucleotides of the at least one sequence are GTA or GTG.

1            12. The isolated polynucleotide sequence according to claim 2, wherein the

polynucleotide sequence comprises more than one copy of at least one sequence selected from the group consisting of SEQ ID NO 24, SEQ ID NO 25, SEQ ID NO 26, SEQ ID NO 27, SEQ ID NO 28, SEQ ID NO 29, SEQ ID NO 30, SEQ ID NO 31, SEQ ID NO 32, SEQ ID NO 33, SEQ ID NO 34, SEQ ID NO 35, and SEQ ID NO 36.

13. A method for identifying and tracking an outbreak of an infection caused by *Enterococcus faecalis*, the method comprising:

- obtaining a sample of a microorganism at a remote facility;
- sequencing a first region of a nucleic acid from the microorganism sample;
- comparing the first sequenced region with historical sequence data stored in a database, the historical sample comprising the sequence of SEQ ID NO 23;
- determining a measure of phylogenetic relatedness between the microorganism sample and a plurality of historical samples stored in the database; and
- providing infection control information based on the phylogenetic relatedness determination to the remote facility, thereby allowing the remote facility to use the infection control information to control or prevent the spread of an infection.

14. An isolated polynucleotide sequence, comprising the sequence of SEQ ID NO 49.

15. An isolated polynucleotide sequence, comprising:

- a region of variable number tandem repeats including at least one copy of SEQ ID NO 50.

1           16. The isolated polynucleotide sequence according to claim 15, wherein the isolated  
2 polynucleotide sequence includes seven copies of SEQ ID NO 50.

1           17. The isolated polynucleotide sequence according to claim 15, further comprising:  
2 at least one point mutation in at least one sequence.

1           18. The isolated polynucleotide sequence according to claim 17, wherein the number of  
2 point mutations is insufficient to prevent identification of the sequence and determination of  
3 phylogenetic relatedness of organisms including the sequence in their genome.

1           19. The isolated polynucleotide sequence according to claim 17, wherein the at least one  
2 point mutation is not in the first three nucleotides of the at least one copy of SEQ ID NO 50.

1           20. The isolated polynucleotide sequence according to claim 15, further comprising:  
2 a forward primer upstream of the sequence; and  
3 a reverse primer downstream of the sequence,  
4 wherein the forward primer and the reverse primer permit identification of the region of  
5 variable number tandem repeats.

1           21. The isolated polynucleotide sequence according to claim 20, wherein the forward  
2 primer comprises SEQ ID NO 51 and the reverse primer comprises SEQ ID NO 52.

1           22. The isolated polynucleotide sequence according to claim 15, wherein the sequence

2 codes for a protein sequence comprising:  
3 at least one copy of SEQ ID NO 53.

1 23. The isolated polynucleotide sequence according to claim 15, wherein the sequence is  
2 isolated from *Helicobacter pylori*.

1 24. The isolated polynucleotide sequence according to claim 15, wherein the first three  
2 nucleotides of the at least one copy of SEQ ID NO 50 are GAT.

1 25. A method for identifying and tracking an outbreak of an infection caused by  
2 *Helicobacter pylori*, the method comprising:  
3 obtaining a sample of a microorganism at a remote facility;  
4 sequencing a first region of a nucleic acid from the microorganism sample;  
5 comparing the first sequenced region with historical sequence data stored in a database,  
6 the historical sample comprising the sequence of SEQ ID NO 50;  
7 determining a measure of phylogenetic relatedness between the microorganism sample  
8 and a plurality of historical samples stored in the database; and  
9 providing infection control information based on the phylogenetic relatedness  
10 determination to the remote facility, thereby allowing the remote facility to use the infection  
11 control information to control or prevent the spread of an infection.

1 26. An isolated polynucleotide sequence, comprising the sequence of SEQ ID NO 54.

1           27. An isolated polynucleotide sequence, comprising:  
2           a region of variable number tandem repeats including at least one sequence selected from  
3 the group consisting of SEQ ID NO 55, SEQ ID NO 56, SEQ ID NO 57, SEQ ID NO 58, SEQ  
4 ID NO 59, SEQ ID NO 60, SEQ ID NO 61, SEQ ID NO 62, SEQ ID NO 63, SEQ ID NO 64,  
5 SEQ ID NO 65, SEQ ID NO 66, SEQ ID NO 67, SEQ ID NO 68, SEQ ID NO 69, SEQ ID NO  
6 70, SEQ ID NO 71, SEQ ID NO 72, SEQ ID NO 73, and SEQ ID NO 74.

1           28. The isolated polynucleotide sequence according to claim 27, further comprising:  
2           at least one point mutation in at least one sequence.

1           29. The isolated polynucleotide sequence according to claim 28, wherein the number of  
2 point mutations is insufficient to prevent identification of the sequence and determination of  
3 phylogenetic relatedness of organisms including the sequence in their genome.

1           30. The isolated polynucleotide sequence according to claim 28, wherein the at least one  
2 point mutation is not in the first three nucleotides of the at least one sequence.

1           31. The isolated polynucleotide sequence according to claim 27, further comprising:  
2 a forward primer upstream of the sequence; and  
3 a reverse primer downstream of the sequence,  
4 wherein the forward primer and the reverse primer permit identification of the region of  
5 variable number tandem repeats.

1           32. The isolated polynucleotide sequence according to claim 31, wherein the forward  
2 primer comprises SEQ ID NO 75 and the reverse primer comprises SEQ ID NO 76.

1           33. The isolated polynucleotide sequence according to claim 27, wherein the sequence  
2 comprises more than one copy of SEQ ID NO 55, SEQ ID NO 56, SEQ ID NO 57, SEQ ID NO  
3 58, SEQ ID NO 59, SEQ ID NO 60, SEQ ID NO 61, SEQ ID NO 62, SEQ ID NO 63, SEQ ID  
4 NO 64, SEQ ID NO 65, SEQ ID NO 66, SEQ ID NO 67, SEQ ID NO 68, SEQ ID NO 69, SEQ  
5 ID NO 70, SEQ ID NO 71, SEQ ID NO 72, SEQ ID NO 73, and SEQ ID NO 74.

1           34. The isolated polynucleotide sequence according to claim 27, wherein the sequence  
2 codes for a protein sequence comprising:  
3           SEQ ID NO 77.

1           35. The isolated polynucleotide sequence according to claim 27, wherein the sequence is  
2 isolated from *Staphylococcus aureus*.

1           36. The isolated polynucleotide sequence according to claim 27, wherein the first three  
2 nucleotides of the at least one sequence are GAT or GAC.

1           37. The isolated polynucleotide sequence according to claim 27, wherein the  
2 polynucleotide sequence comprises more than one copy of at least one sequence selected from  
3 the group consisting of SEQ ID NO 55, SEQ ID NO 56, SEQ ID NO 57, SEQ ID NO 58, SEQ  
4 ID NO 59, SEQ ID NO 60, SEQ ID NO 61, SEQ ID NO 62, SEQ ID NO 63, SEQ ID NO 64,

5 SEQ ID NO 55, SEQ ID NO 66, SEQ ID NO 67, SEQ ID NO 68, SEQ ID NO 69, SEQ ID NO  
6 70, SEQ ID NO 71, SEQ ID NO 72, SEQ ID NO 73, and SEQ ID NO 74.

1 38. A method for identifying and tracking an outbreak of an infection caused by  
2 *Staphylococcus aureus*, the method comprising:  
3 obtaining a sample of a microorganism at a remote facility;  
4 sequencing a first region of a nucleic acid from the microorganism sample;  
5 comparing the first sequenced region with historical sequence data stored in a database,  
6 the historical sample comprising the sequence of SEQ ID NO 54;  
7 determining a measure of phylogenetic relatedness between the microorganism sample  
8 and a plurality of historical samples stored in the database; and  
9 providing infection control information based on the phylogenetic relatedness  
10 determination to the remote facility, thereby allowing the remote facility to use the infection  
11 control information to control or prevent the spread of an infection.

1 39. An isolated polynucleotide sequence, comprising the sequence of SEQ ID NO 54.

1 40. An isolated polynucleotide sequence, comprising:  
2 a region of variable number tandem repeats including at least one sequence selected from  
3 the group consisting of SEQ ID NO 55, SEQ ID NO 56, SEQ ID NO 57, SEQ ID NO 58, SEQ  
4 ID NO 59, SEQ ID NO 60, SEQ ID NO 61, SEQ ID NO 62, SEQ ID NO 63, SEQ ID NO 64,  
5 SEQ ID NO 65, SEQ ID NO 66, SEQ ID NO 67, SEQ ID NO 68, SEQ ID NO 69, SEQ ID NO  
6 70, SEQ ID NO 71, SEQ ID NO 72, SEQ ID NO 78, SEQ ID NO 79, and SEQ ID NO 80.



1           41. The isolated polynucleotide sequence according to claim 40, further comprising:  
2           at least one point mutation in at least one sequence.

1           42. The isolated polynucleotide sequence according to claim 41, wherein the number of  
2 point mutations is insufficient to prevent identification of the sequence and determination of  
3 phylogenetic relatedness of organisms including the sequence in their genome.

1           43. The isolated polynucleotide sequence according to claim 41, wherein the at least one  
2 point mutation is not in the first three nucleotides of the at least one sequence.

1           44. The isolated polynucleotide sequence according to claim 40, further comprising:  
2 a forward primer upstream of the sequence; and  
3 a reverse primer downstream of the sequence;  
4 wherein the forward primer and the reverse primer permit identification of the region of  
5 variable number tandem repeats.

1           45. The isolated polynucleotide sequence according to claim 44, wherein the forward  
2 primer comprises SEQ ID NO 76 and the reverse primer comprises SEQ ID NO 77.

1           46. The isolated polynucleotide sequence according to claim 40, wherein the sequence  
2 comprises more than one copy of SEQ ID NO 55, SEQ ID NO 56, SEQ ID NO 57, SEQ ID NO  
3 58, SEQ ID NO 59, SEQ ID NO 60, SEQ ID NO 61, SEQ ID NO 62, SEQ ID NO 63, SEQ ID

4 NO 64, SEQ ID NO 65, SEQ ID NO 66, SEQ ID NO 67, SEQ ID NO 68, SEQ ID NO 69, SEQ  
5 ID NO 70, SEQ ID NO 71, SEQ ID NO 72, SEQ ID NO 78, SEQ ID NO 79, and SEQ ID NO  
6 80.

1 47. The isolated polynucleotide sequence according to claim 40, wherein the sequence is  
2 isolated from *Staphylococcus aureus*.

1 48. The isolated polynucleotide sequence according to claim 40, wherein the first three  
2 nucleotides of the at least one sequence are GAT or GAC.

1 49. The isolated polynucleotide sequence according to claim 40, wherein the  
2 polynucleotide sequence comprises more than one copy of at least one sequence selected from  
3 the group consisting of SEQ ID NO 55, SEQ ID NO 56, SEQ ID NO 57, SEQ ID NO 58, SEQ  
4 ID NO 59, SEQ ID NO 60, SEQ ID NO 61, SEQ ID NO 62, SEQ ID NO 63, SEQ ID NO 64,  
5 SEQ ID NO 65, SEQ ID NO 66, SEQ ID NO 67, SEQ ID NO 68, SEQ ID NO 69, SEQ ID NO  
6 70, SEQ ID NO 71, SEQ ID NO 72, SEQ ID NO 78, SEQ ID NO 79, and SEQ ID NO 80.

1 50. A method for identifying and tracking an outbreak of an infection caused by  
2 *Staphylococcus aureus*, the method comprising:  
3 obtaining a sample of a microorganism at a remote facility;  
4 sequencing a first region of a nucleic acid from the microorganism sample;  
5 comparing the first sequenced region with historical sequence data stored in a database,  
6 the historical sample comprising the sequence of SEQ ID NO 54;

7           determining a measure of phylogenetic relatedness between the microorganism sample  
8   and a plurality of historical samples stored in the database; and  
9           providing infection control information based on the phylogenetic relatedness  
10   determination to the remote facility, thereby allowing the remote facility to use the infection  
11   control information to control or prevent the spread of an infection.